

1288495
SEQUENCE LISTING

<110> Cambridge University Technical Services Limited
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Della, Marina
Weller, Geoffrey
Jackson, Stephen

<120> Prokaryotic DNA Repair Ligases

<130> 6947-73362-01

<140> US 10/568,055

<141> 2006-02-10

<150> PCT/GB2004/003349

<151> 2004-08-02

<150> US 60/494,088

<151> 2003-08-12

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<170> PatentIn version 3.1

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35 40 45

Ala Thr Arg Lys Arg Trp Pro Asn Gly Val Asp Gln Pro Ala Phe Phe
50 55 60

Glu Lys Gln Leu Ala Leu Ser Ala Pro Pro Trp Leu Ser Arg Ala Thr
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 325 330 335

His Tyr Asp Phe Arg Leu Glu Cys Asp Gly Val Leu Val Ser Trp Ala
 340 345 350

Val Pro Lys Asn Leu Pro Asp Asn Thr Ser Val Asn His Leu Ala Ile
 355 360 365

His Thr Glu Asp His Pro Leu Glu Tyr Ala Thr Phe Glu Gly Ala Ile
 370 375 380

Pro Ser Gly Glu Tyr Gly Ala Gly Lys Val Ile Ile Trp Asp Ser Gly
 385 390 395 400

Thr Tyr Asp Thr Glu Lys Phe His Asp Asp Pro His Thr Gly Glu Val
 405 410 415

Ile Val Asn Leu His Gly Gly Arg Ile Ser Gly Arg Tyr Ala Leu Ile
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Arg Thr Asn Gly Asp Arg Trp Leu Ala His Arg Leu Lys Asn Gln Lys
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Asp Gln Lys Val Phe Glu Phe Asp Asn Leu Ala Pro Met Leu Ala Thr
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His Gly Thr Val Ala Gly Leu Lys Ala Ser Gln Trp Ala Phe Glu Gly
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Lys Trp Asp Gly Tyr Arg Leu Leu Val Glu Ala Asp His Gly Ala Val
 485 490 495

Arg Leu Arg Ser Arg Ser Gly Arg Asp Val Thr Ala Glu Tyr Pro Gln
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Leu Arg Ala Leu Ala Glu Asp Leu Ala Asp His His Val Val Leu Asp
 515 520 525

Gly Glu Ala Val Val Leu Asp Ser Ser Gly Val Pro Ser Phe Ser Gln
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Met Gln Asn Arg Gly Arg Asp Thr Arg Val Glu Phe Trp Ala Phe Asp
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Leu Leu Tyr Leu Asp Gly Arg Ala Leu Leu Gly Thr Arg Tyr Gln Asp
 565 570 575

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Arg Arg Lys Leu Leu Glu Thr Leu Ala Asn Ala Thr Ser Leu Thr Val
580 585 590

Pro Glu Leu Leu Pro Gly Asp Gly Ala Gln Ala Phe Ala Cys Ser Arg
595 600 605

Lys His Gly Trp Glu Gly Val Ile Ala Lys Arg Arg Asp Ser Arg Tyr
610 615 620

Gln Pro Gly Arg Arg Cys Ala Ser Trp Val Lys Asp Lys His Trp Asn
625 630 635 640

Thr Gln Glu Val Val Ile Gly Gly Trp Arg Ala Gly Glu Gly Gly Arg
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Ser Ser Gly Val Gly Ser Leu Leu Met Gly Ile Pro Gly Pro Gly Gly
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Leu Gln Phe Ala Gly Arg Val Gly Thr Gly Leu Ser Glu Arg Glu Leu
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Ala Asn Leu Lys Glu Met Leu Ala Pro Leu His Thr Asp Glu Ser Pro
690 695 700

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Lys Pro Ala Leu Val Ala Glu Val Arg Tyr Ser Glu Trp Thr Pro Glu
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Gln Val His Ala Lys Asp Asn Gly Arg Ile Arg Tyr Lys Arg Val Cys
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Glu Ala Cys Gly Glu Val Val Asp Tyr Arg Asp Leu Ala Arg Ala Tyr
50 55 60

Glu Ser Gly Asp Gly Gln Met Val Ala Ile Thr Asp Asp Asp Ile Ala
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85 90 95

Pro Ala Ala Asp Val Asp Pro Met Met Phe Asp Arg Ser Tyr Phe Leu
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Glu Pro Asp Ser Lys Ser Ser Lys Ser Tyr Val Leu Leu Ala Lys Thr
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Leu Ala Glu Thr Asp Arg Met Ala Ile Val His Phe Thr Leu Arg Asn
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Lys Thr Arg Leu Ala Ala Leu Arg Val Lys Asp Phe Gly Lys Arg Glu
145 150 155 160

Val Met Met Val His Thr Leu Leu Trp Pro Asp Glu Ile Arg Asp Pro
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Lys Met Ala Gly Gln Val Val Asp Ser Met Ala Asp Asp Phe Asn Pro
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210 215 220

Thr Lys Leu Glu Gly Gly Gln Ala Phe Thr Ala Glu Asp Gln Pro Arg
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Leu Leu Asp Glu Pro Glu Asp Val Ser Asp Leu Leu Ala Lys Leu Glu
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Ala Ser Val Lys Ala Arg Ser Lys Ala Asn Ser Asn Val Pro Thr Pro
260 265 270

Pro

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